

OP1741seqUS
SEQUENCE LISTING

<110>

<120> Method for producing L-arginine or L-lysine by fermentation

<130>

<150> JP 2003-
<151> 2003-03-03

<160> 24

<170> PatentIn Ver. 2.0

<210> 1
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<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer for PCR

<400> 1
cccggtttt cttctgcaac tcggg

25

<210> 2
<211> 25
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer for PCR

<400> 2
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25

<210> 3
<211> 24
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer for PCR

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24

<210> 4
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<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer for PCR

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25

<210> 5
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<212> DNA
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<220>
<223> Description of Artificial Sequence: primer

<400> 5
agaactacga gtccgccttt ttg 23

<210> 6
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<220>
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<220>
<223> Description of Artificial Sequence: primer

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<210> 8
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<220>
<223> Description of Artificial Sequence: primer

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<210> 9
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<220>
<223> Description of Artificial Sequence: primer

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<210> 10
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<220>
<223> Description of Artificial Sequence: primer

<400> 10
cggcgagacc gtcgattggg aggagc 26

<210> 11

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<211> 22
<212> DNA
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<220>
<223> Description of Artificial Sequence: primer

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<210> 12
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<212> DNA
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<220>
<223> Description of Artificial Sequence: primer

<400> 12
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<210> 13
<211> 23
<212> DNA
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<220>
<223> Description of Artificial Sequence: primer

<400> 13
gccccgggca ggcaagaatc ctc 23

<210> 14
<211> 21
<212> DNA
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<220>
<223> Description of Artificial Sequence: primer

<400> 14
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<210> 15
<211> 4235
<212> DNA
<213> Brevibacterium flavum

<220>
<221> CDS
<222> (1852)..(2364)

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tgggttccct cgcgcgtact ggccagccag acaagcgtga agcgttctg ccaatgccaa 180
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cagcacctga aggattccctc aaggcagtgc gcgagctgtg cgatgagttac ggcatacttga 360
tgatcaccga tgaagtccag actggcgttg gccgtaccgg cgatttctt gcacatcagc 420
acgatggcgt tggcccgtat gtggtgacca tggccaaaggg acttggcggc ggtcttccca 480
tcgggtgttg tttggccact ggccgtgcag ctgaatttgc gaccccaggc aagcacggca 540
ccactttcgg tggcaaccca gttgttgtg cagctgcac ggcagtgtcg tctgttgtcg 600

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gctaacgacg	gcccacatctt	cctgcactgc	tttcctgcct	accgcggcaa	agaagtggca	1740
gcctccgtga	ttgatggacc	agcgtccaaa	gtttcgtatg	aagcagaaaa	ccgcctccac	1800
gctcagaaag	cactgcttgt	gtggctgctg	gccaaccaggc	cgaggttaaga	c atg tct	1857

Met Ser

1

ctt ggc tca acc ccg tca aca ccg gaa aac tta aat ccc	gtg act cgc	1905
Leu Gly Ser Thr Pro Ser Thr Pro Glu Asn Leu Asn Pro Val	Thr Arg	
5 10 15		
act gca cgc caa gct ctc att ttg cag att ttg gac aaa	caa aaa gtc	1953
Thr Ala Arg Gln Ala Leu Ile Leu Gln Ile Leu Asp Lys	Gln Lys Val	
20 25 30		
acc agc cag gta caa ctg tct gaa ttg ctg ctg gat gaa	ggc atc gat	2001
Thr Ser Gln Val Gln Leu Ser Glu Leu Leu Leu Asp Glu	Gly Ile Asp	
35 40 45 50		
atc acc cag gcc acc ttg tcc cgg gat ctc gat gaa ctc	ggt gca cgc	2049
Ile Thr Gln Ala Thr Leu Ser Arg Asp Leu Asp Glu Leu	Gly Ala Arg	
55 60 65		
aag gtt cgc ccc gat ggg gga cgc gcc tac tac gcg gtc	ggc cca gta	2097
Lys Val Arg Pro Asp Gly Gly Arg Ala Tyr Tyr Ala Val	Gly Pro Val	
70 75 80		
gat agc atc gcc cgc gaa gat ctc cgg ggt ccg tcg gag	aag ctg cgc	2145
Asp Ser Ile Ala Arg Glu Asp Leu Arg Gly Pro Ser Glu	Lys Leu Arg	
85 90 95		
cgc atg ctt gat gaa ctg ctg gtt tct aca gat cat tcc	ggc aac atc	2193
Arg Met Leu Asp Glu Leu Leu Val Ser Thr Asp His Ser	Gly Asn Ile	
100 105 110		
gct atg ctg cgc acc ccg ccc gga gct gcc cag tac ctg	gca agt ttc	2241
Ala Met Leu Arg Thr Pro Pro Gly Ala Ala Gln Tyr Leu	Ala Ser Phe	
115 120 125 130		
atc gat agg gtg ggg ctg aaa gaa gtc gtt ggc acc atc	gct ggc gat	2289
Ile Asp Arg Val Gly Leu Lys Glu Val Val Gly Thr Ile	Ala Gly Asp	
135 140 145		
gac acc gtt ttt gtt ctc gcc cgt gat ccg ctc aca ggt	aaa gaa cta	2337
Asp Thr Val Phe Val Leu Ala Arg Asp Pro Leu Thr Gly	Lys Glu Leu	
150 155 160		
ggt gaa tta ctc agc ggg cgc acc act taaagcgccc	ctagttcaag	2384
Gly Glu Leu Leu Ser Gly Arg Thr Thr		
165 170		
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gcattggatg cccgtgcagc tgagtccatc gttgttgatg	caaaggatga gttcgctgag	2744
gagtactgccc tgccaaaccat caaggcAACAC ggcatgtaca	tgaagcgtt cccactgggt	2804

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agaactcaa	gtat	tagaa	caccatgg	aacagcacgg	aaccaatgaa	3824
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gccaagg	tgcacca	agactactt	tctgatgaa	atctagcc	catgctgg	4004
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gaggatgtgc	acggcg	gaaac	ctgattgacc	gcgttgg	tgaggtgg	4124
ggccgtctgc	gcatcg	ttcccg	gaccagg	caacc	ccgcatgt	4184
gtccgcac	catcg	catcg	ggaacaacc	agcttgc	c	4235

<210> 16
<211> 171
<212> PRT
<213> *Brevibacterium flavum*

<400> 16

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Thr	Arg	Thr	Ala	Arg	Gln	Ala	Leu	Ile	Leu	Gln	Ile	Leu	Asp	Lys	Gln
								20		25				30	
Lys	Val	Thr	Ser	Gln	Val	Gln	Leu	Ser	Glu	Leu	Leu	Leu	Asp	Glu	Gly
								35		40				45	
Ile	Asp	Ile	Thr	Gln	Ala	Thr	Leu	Ser	Arg	Asp	Leu	Asp	Glu	Leu	Gly
								50		55				60	
Ala	Arg	Lys	Val	Arg	Pro	Asp	Gly	Gly	Arg	Ala	Tyr	Tyr	Ala	Val	Gly
								65		70				80	
Pro	Val	Asp	Ser	Ile	Ala	Arg	Glu	Asp	Leu	Arg	Gly	Pro	Ser	Glu	Lys
								85		90				95	
Leu	Arg	Arg	Met	Leu	Asp	Glu	Leu	Leu	Val	Ser	Thr	Asp	His	Ser	Gly
								100		105				110	
Asn	Ile	Ala	Met	Leu	Arg	Thr	Pro	Pro	Gly	Ala	Ala	Gln	Tyr	Leu	Ala
								115		120				125	
Ser	Phe	Ile	Asp	Arg	Val	Gly	Leu	Lys	Glu	Val	Val	Gly	Thr	Ile	Ala
								130		135				140	
Gly	Asp	Asp	Thr	Val	Phe	Val	Leu	Ala	Arg	Asp	Pro	Leu	Thr	Gly	Lys
								145		150				155	
Glu	Leu	Gly	Glu	Leu	Leu	Ser	Gly	Arg	Thr	Thr					160
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<210> 17
<211> 3138
<212> DNA
<213> *Brevibacterium lactofermentum*

<220>
<221> CDS
<222> (1)..(3138)

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<400> 17

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gac cca ctg cca aaa gtt ggt tct tta tcg ctg aaa tct gag cat gcc	96
Asp Pro Leu Pro Lys Val Gly Ser Leu Ser Leu Lys Ser Glu His Ala	
20 25 30	
caa gca gat cta gag cat ttg ggt tgg cgc aat gtt gag tct ttg gat	144
Gln Ala Asp Leu Glu His Leu Gly Trp Arg Asn Val Glu Ser Leu Asp	
35 40 45	
ttg ttg tgg ggc ttg tca ggt gca ggc gat ccc gat gtc gcg ctg aac	192
Leu Leu Trp Gly Leu Ser Gly Ala Gly Asp Pro Asp Val Ala Leu Asn	
50 55 60	
ctt ctt att cgg ctg tat cag gca ctt gaa gca atc ggc gag gat gct	240
Leu Leu Ile Arg Leu Tyr Gln Ala Leu Glu Ala Ile Gly Glu Asp Ala	
65 70 75 80	
cga aac gag ctt gat caa gag att cgc cag gat gaa gaa cta cga gtc	288
Arg Asn Glu Leu Asp Gln Glu Ile Arg Gln Asp Glu Glu Leu Arg Val	
85 90 95	
cgc ctt ttt gca ttg ttg ggt ggt tcc tcg gct gtc ggt gat cac ttg	336
Arg Leu Phe Ala Leu Leu Gly Gly Ser Ser Ala Val Gly Asp His Leu	
100 105 110	
gtc gcc aat cct ttg cag tgg aaa ctc tta aaa ctt gat gcg cca tcg	384
Val Ala Asn Pro Leu Gln Trp Lys Leu Lys Leu Asp Ala Pro Ser	
115 120 125	
agg gaa gag atg ttt cag gcg ctg ctg gaa tct gtg aaa gct cag cct	432
Arg Glu Glu Met Phe Gln Ala Leu Leu Glu Ser Val Lys Ala Gln Pro	
130 135 140	
gct gtg ctt gag gtt gag gat ttc agc gat gca cac aac att gcc cga	480
Ala Val Leu Glu Val Glu Asp Phe Ser Asp Ala His Asn Ile Ala Arg	
145 150 155 160	
gac gat ttg agc acg cct ggt ttt tac acg gct agt gtt acc ggg cct	528
Asp Asp Leu Ser Thr Pro Gly Phe Tyr Thr Ala Ser Val Thr Gly Pro	
165 170 175	
gaa gca gag cga gtc ttg aaa tgg act tat cgc acg ttg ctg acc cgg	576
Glu Ala Glu Arg Val Leu Lys Trp Thr Tyr Arg Thr Leu Leu Thr Arg	
180 185 190	
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Ile Ala Ala His Asp Leu Ala Gly Thr Tyr Pro Thr Asp Met Arg Arg	
195 200 205	
aaa ggt ggc gat cct gtt ccg ttt agc aca gtg acc atg cag ctc agc	672
Lys Gly Gly Asp Pro Val Pro Phe Ser Thr Val Thr Met Gln Leu Ser	
210 215 220	
gac cta gct gat gct gct ttg act gct gct tta gct gtg gca att gcc	720
Asp Leu Ala Asp Ala Ala Leu Thr Ala Ala Leu Ala Val Ala Ile Ala	
225 230 235 240	
aat gtt tat ggt gaa aag ccg gtt gat tca gct tta tct gtc atc gcg	768
Asn Val Tyr Gly Glu Lys Pro Val Asp Ser Ala Leu Ser Val Ile Ala	
245 250 255	
atg ggc aaa tgt ggc gcg cag gaa ttg aac tac att tca gat gtg gac	816
Met Gly Lys Cys Gly Ala Gln Glu Leu Asn Tyr Ile Ser Asp Val Asp	
260 265 270	
gtg gtg ttt gtt gca gag ccg gca aac tct aaa tca aca cgc acc gca	864
Val Val Phe Val Ala Glu Pro Ala Asn Ser Lys Ser Thr Arg Thr Ala	
275 280 285	
gca gag ctc att cgc atc ggt agc aac tcg ttc ttt gag gtg gat gca	912
Ala Glu Leu Ile Arg Ile Gly Ser Asn Ser Phe Phe Glu Val Asp Ala	
290 295 300	
gca ctt cgc cca gaa ggt aaa agt ggc gct ctt gtg cgc tct ttg gat	960
Ala Leu Arg Pro Glu Gly Lys Ser Gly Ala Leu Val Arg Ser Leu Asp	
305 310 315 320	
tcc cat atg gcg tat tac aag cgc tgg gcg gaa acc tgg gaa ttt cag	1008
Ser His Met Ala Tyr Tyr Lys Arg Trp Ala Glu Thr Trp Glu Phe Gln	

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Ala	Leu	Leu	Lys	Ala	Arg	Pro	Met	Thr	Gly	Asp	Ile	Asp	Leu	Gly	Gln
325	330	335													
340	345	350													
tcc	tat	gtg	gat	gct	ctt	tca	ccg	ttg	att	tgg	gcg	gct	agc	cag	cgg
Ser	Tyr	Val	Asp	Ala	Leu	Ser	Pro	Leu	Ile	Trp	Ala	Ala	Ser	Gln	Arg
355	360	365													
gaa	tca	ttt	gtc	aca	gat	gtc	caa	gct	atg	cgc	cgt	cga	gtg	ttg	gac
Glu	Ser	Phe	Val	Thr	Asp	Val	Gln	Ala	Met	Arg	Arg	Arg	Val	Leu	Asp
370	375	380													
aat	gtt	ccg	gaa	gac	ttg	cgt	gat	cgt	gag	ctg	aag	ctt	ggg	cgc	ggt
Asn	Val	Pro	Glu	Asp	Leu	Arg	Asp	Arg	Glu	Leu	Lys	Leu	Gly	Arg	Gly
385	390	395													
ggt	ttg	agg	gat	gtg	gag	ttt	gct	gtc	cag	ctc	ctt	cag	atg	gtg	cat
Gly	Leu	Arg	Asp	Val	Glu	Phe	Ala	Val	Gln	Leu	Leu	Gln	Met	Val	His
405	410	415													
ggt	cgc	att	gat	gag	acg	ttg	cgg	gtt	cgg	tca	acg	gta	aat	gct	ttg
Gly	Arg	Ile	Asp	Glu	Thr	Leu	Arg	Val	Arg	Ser	Thr	Val	Asn	Ala	Leu
420	425	430													
cat	gtg	ttg	ttt	gat	cag	gga	tat	gtg	ggt	cgt	gaa	gac	ggg	cat	aat
His	Val	Leu	Val	Asp	Gln	Gly	Tyr	Val	Gly	Arg	Glu	Asp	Gly	His	Asn
435	440	445													
ctc	att	gag	tcg	tat	gag	ttt	ttg	cgc	ctg	ttg	gag	cat	cgc	ctt	caa
Leu	Ile	Glu	Ser	Tyr	Glu	Phe	Leu	Arg	Leu	Leu	Glu	His	Arg	Leu	Gln
450	455	460													
ttg	gag	cg	atc	aag	cgc	act	cac	ttg	tta	ccg	aaa	cct	gat	gac	cga
Leu	Glu	Arg	Ile	Lys	Arg	Thr	His	Leu	Leu	Pro	Lys	Pro	Asp	Asp	Arg
465	470	475													
atg	aat	atg	cgc	tgg	ttg	gcg	cgc	gct	tct	ggg	ttt	act	ggt	tcg	atg
Met	Asn	Met	Arg	Trp	Leu	Ala	Arg	Ala	Ser	Gly	Phe	Thr	Gly	Ser	Met
485	490	495													
gag	caa	agt	tcg	gcc	aaa	gct	atg	gaa	cgg	cat	ttg	cgt	aag	gtt	cgt
Glu	Gln	Ser	Ser	Ala	Lys	Ala	Met	Glu	Arg	His	Leu	Arg	Lys	Val	Arg
500	505	510													
ttg	cag	att	cag	tcg	ttg	cat	agt	cag	ctg	ttt	tat	cgg	cca	ctg	ctg
Leu	Gln	Ile	Gln	Ser	Leu	His	Ser	Gln	Leu	Phe	Tyr	Arg	Pro	Leu	Leu
515	520	525													
aac	tct	gtg	gtc	aac	ttg	agc	gcg	gat	gcc	atc	aga	ttg	tct	ccg	gat
Asn	Ser	Val	Val	Asn	Leu	Ser	Ala	Asp	Ala	Ile	Arg	Leu	Ser	Pro	Asp
530	535	540													
gct	gca	aag	cta	caa	ttg	ggg	gca	ttg	gga	tac	ctg	cat	cca	tca	cgt
Ala	Ala	Lys	Leu	Gln	Leu	Gly	Ala	Leu	Gly	Tyr	Leu	His	Pro	Ser	Arg
545	550	555													
gct	tat	gaa	cac	ctg	act	gct	ctt	gca	tca	gga	gct	agc	cgt	aaa	gcc
Ala	Tyr	Glu	His	Leu	Thr	Ala	Leu	Ala	Ser	Gly	Ala	Ser	Arg	Lys	Ala
565	570	575													
aag	att	cag	gcg	atg	ttg	ctg	ccc	acg	ttg	atg	gag	tgg	ctg	tct	caa
Lys	Ile	Gln	Ala	Met	Leu	Leu	Pro	Thr	Leu	Met	Glu	Trp	Leu	Ser	Gln
580	585	590													
aca	gct	gaa	cca	gat	gcg	gga	ttg	ctg	aat	tac	cgc	aag	ctt	tct	gat
Thr	Ala	Glu	Pro	Asp	Ala	Gly	Leu	Leu	Asn	Tyr	Arg	Lys	Leu	Ser	Asp
595	600	605													
gct	tcc	tat	gat	cgc	agc	tgg	ttt	ttg	cgc	atg	ctg	cgt	gat	gag	ggc
Ala	Ser	Tyr	Asp	Arg	Ser	Trp	Phe	Leu	Arg	Met	Leu	Arg	Asp	Glu	Gly
610	615	620													
gta	gtg	ggg	cag	cgg	ttg	atg	cgt	att	tgg	gga	aat	tct	ccc	tat	att
Val	Val	Gly	Gln	Arg	Leu	Met	Arg	Ile	Leu	Gly	Asn	Ser	Pro	Tyr	Ile
625	630	635													
tct	gaa	ctg	att	atc	tcc	act	ccg	gac	ttt	gtg	aaa	cag	ctg	ggt	gat
Ser	Glu	Leu	Ile	Ile	Ser	Thr	Pro	Asp	Phe	Val	Lys	Gln	Leu	Gly	Asp
645	650	655													
gcg	gcf	tct	ggt	cct	aaa	ttg	ctt	gct	act	gca	ccg	act	cag	gtt	gtg
Ala	Ala	Ser	Gly	Pro	Lys	Leu	Leu	Ala	Thr	Ala	Pro	Thr	Gln	Val	Val

OP1741seqUS															
	660		665		670										
aaa gca atc aag gcg acg gtg tcg cgt cat gag tca cct gat cg ^g g ^c g ^c g ^c															2064
Lys Ala Ile Lys Ala Thr Val Ser Arg His Glu Ser Pro Asp Arg Ala	675	680	685												
atc cag gct gca cga tcg ctg agg agg cag gag ctg gca cgc att gcc															2112
Ile Gln Ala Ala Arg Ser Leu Arg Arg Gln Glu Leu Ala Arg Ile Ala	690	695	700												
tct gct gat ttg ctc aac atg ctc act gtt cag gaa gta tgc caa agc															2160
Ser Ala Asp Leu Leu Asn Met Leu Thr Val Gln Glu Val Cys Gln Ser	705	710	715	720											
ttg tca cta gtc tgg gat gcg gtg ttg gat gct gcc ttg gat g ^c g ^a gaa															2208
Leu Ser Leu Val Trp Asp Ala Val Leu Asp Ala Ala Leu Asp Ala Glu	725	730	735												
atc cgt gct gca ctt aac gat cca cag aaa cca gat cag cct ctg gcc															2256
Ile Arg Ala Ala Leu Asn Asp Pro Gln Lys Pro Asp Gln Pro Leu Ala	740	745	750												
aat att tct gtg atc ggc atg ggc cgt ttg ggt gga gca gaa ctt gga															2304
Asn Ile Ser Val Ile Gly Met Gly Arg Leu Gly Gly Ala Glu Leu Gly	755	760	765												
tac ggt tct gat gcc gat gtg atg ttt gta tgc gag ccg gta gcc ggt															2352
Tyr Gly Ser Asp Ala Asp Val Met Phe Val Cys Glu Pro Val Ala Gly	770	775	780												
gtg gaa gag cat gag gcc gtc aca tgg tct att gcg atc tgt gat tcc															2400
Val Glu Glu His Glu Ala Val Thr Trp Ser Ile Ala Ile Cys Asp Ser	785	790	795	800											
atg cgg tcg agg ctt gcg cag cct tcc ggt gat cca cct ttg gag gtg															2448
Met Arg Ser Arg Leu Ala Gln Pro Ser Gly Asp Pro Pro Leu Glu Val	805	810	815												
gat ctg ggg ctg cgt cct gaa ggg aga tct ggt g ^c g ^c acc															2496
Asp Leu Gly Leu Arg Pro Glu Gly Arg Ser Gly Ala Ile Val Arg Thr	820	825	830												
gtt gat tcc tat gtg aag tac tac gaa aag tgg ggt gaa act tgg gag															2544
Val Asp Ser Tyr Val Lys Tyr Glu Lys Trp Gly Glu Thr Trp Glu	835	840	845												
att cag gcg ctg ctg agg gct gcg tgg gtt gct ggt gat cgt gag ctg															2592
Ile Gln Ala Leu Leu Arg Ala Ala Trp Val Ala Gly Asp Arg Glu Leu	850	855	860												
ggc att aag ttc ttg gag tcg att gat cgt ttc cgc tac cca gtt gac															2640
Gly Ile Lys Phe Leu Glu Ser Ile Asp Arg Phe Arg Tyr Pro Val Asp	865	870	875	880											
ggg gca acg cag gc ^g cag ctt cgt gaa gtt cgt cga att aag g ^c g ^c agg															2688
Gly Ala Thr Gln Ala Gln Leu Arg Glu Val Arg Arg Ile Lys Ala Arg	885	890	895												
gtg gat aat gag agg ctt ccg cgc ggg gct gat cga aat acc cat acc															2736
Val Asp Asn Glu Arg Leu Pro Arg Gly Ala Asp Arg Asn Thr His Thr	900	905	910												
aag ctg ggt cgg gga gc ^g tta act gac atc gag tgg act gtg cag ttg															2784
Lys Leu Gly Arg Gly Ala Leu Thr Asp Ile Glu Trp Thr Val Gln Leu	915	920	925												
ttg acc atg atg cat gct cat gag att ccg gag ctg cac aat acg tcg															2832
Leu Thr Met Met His Ala His Glu Ile Pro Glu Leu His Asn Thr Ser	930	935	940												
acg ttg gaa gtt ctt gaa gtg ctg gaa aag cat cag att att aac cct															2880
Thr Leu Glu Val Leu Glu Val Leu Glu Lys His Gln Ile Ile Asn Pro	945	950	955	960											
gtg cag gtg cag acg ctt cgg gaa gc ^g tgg ctg acg gca acg gct gct															2928
Val Gln Val Gln Thr Leu Arg Glu Ala Trp Leu Thr Ala Thr Ala Ala	965	970	975												
agg aat gc ^g ctt gtg ctg gtc agg ggt aag aga tta gat cag tta cct															2976
Arg Asn Ala Leu Val Leu Val Arg Gly Lys Arg Leu Asp Gln Leu Pro	980	985	990												
act cct ggt ccg cac ctt gc ^g cag gtg gct ggt gc ^g tct ggt tgg gat															3024
Thr Pro Gly Pro His Leu Ala Gln Val Ala Gly Ala Ser Gly Trp Asp															

OP1741seqUS

995 cca aat gag tac cag gag tat ttg gaa aac tat ctg aaa gtg acc agg Pro Asn Glu Tyr Gln Glu Tyr Leu Glu Asn Tyr Leu Lys Val Thr Arg 1010 aag agt cgt cag gtt gat gaa gtc ttc tgg ggt gtg gac tct atg Lys Ser Arg Gln Val Val Asp Glu Val Phe Trp Gly Val Asp Ser Met 1025 gag caa cgt gag ttt tag Glu Gln Arg Glu Phe 1045	1000 1015 1020 1030 1035 1040	1005 3072 3120 3138
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<210> 18

<211> 1045

<212> PRT

<213> *Brevibacterium lactofermentum*

<400> 18

Met Ser Gly Pro Leu Arg Ser Glu Arg Lys Val Val Gly Phe Val Arg	1	5	10	15
Asp Pro Leu Pro Lys Val Gly Ser Leu Ser Leu Lys Ser Glu His Ala	20	25	30	
Gln Ala Asp Leu Glu His Leu Gly Trp Arg Asn Val Glu Ser Leu Asp	35	40	45	
Leu Leu Trp Gly Leu Ser Gly Ala Gly Asp Pro Asp Val Ala Leu Asn	50	55	60	
Leu Leu Ile Arg Leu Tyr Gln Ala Leu Glu Ala Ile Gly Glu Asp Ala	65	70	75	80
Arg Asn Glu Leu Asp Gln Glu Ile Arg Gln Asp Glu Glu Leu Arg Val	85	90	95	
Arg Leu Phe Ala Leu Leu Gly Gly Ser Ser Ala Val Gly Asp His Leu	100	105	110	
Val Ala Asn Pro Leu Gln Trp Lys Leu Leu Lys Leu Asp Ala Pro Ser	115	120	125	
Arg Glu Glu Met Phe Gln Ala Leu Leu Glu Ser Val Lys Ala Gln Pro	130	135	140	
Ala Val Leu Glu Val Glu Asp Phe Ser Asp Ala His Asn Ile Ala Arg	145	150	155	160
Asp Asp Leu Ser Thr Pro Gly Phe Tyr Thr Ala Ser Val Thr Gly Pro	165	170	175	
Glu Ala Glu Arg Val Leu Lys Trp Thr Tyr Arg Thr Leu Leu Thr Arg	180	185	190	
Ile Ala Ala His Asp Leu Ala Gly Thr Tyr Pro Thr Asp Met Arg Arg	195	200	205	
Lys Gly Gly Asp Pro Val Pro Phe Ser Thr Val Thr Met Gln Leu Ser	210	215	220	
Asp Leu Ala Asp Ala Ala Leu Thr Ala Ala Leu Ala Val Ala Ile Ala	225	230	235	240
Asn Val Tyr Gly Glu Lys Pro Val Asp Ser Ala Leu Ser Val Ile Ala	245	250	255	
Met Gly Lys Cys Gly Ala Gln Glu Leu Asn Tyr Ile Ser Asp Val Asp	260	265	270	
Val Val Phe Val Ala Glu Pro Ala Asn Ser Lys Ser Thr Arg Thr Ala	275	280	285	
Ala Glu Leu Ile Arg Ile Gly Ser Asn Ser Phe Phe Glu Val Asp Ala	290	295	300	
Ala Leu Arg Pro Glu Gly Lys Ser Gly Ala Leu Val Arg Ser Leu Asp	305	310	315	320
Ser His Met Ala Tyr Tyr Lys Arg Trp Ala Glu Thr Trp Glu Phe Gln	325	330	335	
Ala Leu Leu Lys Ala Arg Pro Met Thr Gly Asp Ile Asp Leu Gly Gln	340	345	350	
Ser Tyr Val Asp Ala Leu Ser Pro Leu Ile Trp Ala Ala Ser Gln Arg	355	360	365	

OP1741seqUS

Glu Ser Phe Val Thr Asp Val Gln Ala Met Arg Arg Arg Val Leu Asp
 370 375 380
 Asn Val Pro Glu Asp Leu Arg Asp Arg Glu Leu Lys Leu Gly Arg Gly
 385 390 395 400
 Gly Leu Arg Asp Val Glu Phe Ala Val Gln Leu Leu Gln Met Val His
 405 410 415
 Gly Arg Ile Asp Glu Thr Leu Arg Val Arg Ser Thr Val Asn Ala Leu
 420 425 430
 His Val Leu Val Asp Gln Gly Tyr Val Gly Arg Glu Asp Gly His Asn
 435 440 445
 Leu Ile Glu Ser Tyr Glu Phe Leu Arg Leu Leu Glu His Arg Leu Gln
 450 455 460
 Leu Glu Arg Ile Lys Arg Thr His Leu Leu Pro Lys Pro Asp Asp Arg
 465 470 475 480
 Met Asn Met Arg Trp Leu Ala Arg Ala Ser Gly Phe Thr Gly Ser Met
 485 490 495
 Glu Gln Ser Ser Ala Lys Ala Met Glu Arg His Leu Arg Lys Val Arg
 500 505 510
 Leu Gln Ile Gln Ser Leu His Ser Gln Leu Phe Tyr Arg Pro Leu Leu
 515 520 525
 Asn Ser Val Val Asn Leu Ser Ala Asp Ala Ile Arg Leu Ser Pro Asp
 530 535 540
 Ala Ala Lys Leu Gln Leu Gly Ala Leu Gly Tyr Leu His Pro Ser Arg
 545 550 555 560
 Ala Tyr Glu His Leu Thr Ala Leu Ala Ser Gly Ala Ser Arg Lys Ala
 565 570 575
 Lys Ile Gln Ala Met Leu Leu Pro Thr Leu Met Glu Trp Leu Ser Gln
 580 585 590
 Thr Ala Glu Pro Asp Ala Gly Leu Leu Asn Tyr Arg Lys Leu Ser Asp
 595 600 605
 Ala Ser Tyr Asp Arg Ser Trp Phe Leu Arg Met Leu Arg Asp Glu Gly
 610 615 620
 Val Val Gly Gln Arg Leu Met Arg Ile Leu Gly Asn Ser Pro Tyr Ile
 625 630 635 640
 Ser Glu Leu Ile Ile Ser Thr Pro Asp Phe Val Lys Gln Leu Gly Asp
 645 650 655
 Ala Ala Ser Gly Pro Lys Leu Leu Ala Thr Ala Pro Thr Gln Val Val
 660 665 670
 Lys Ala Ile Lys Ala Thr Val Ser Arg His Glu Ser Pro Asp Arg Ala
 675 680 685
 Ile Gln Ala Ala Arg Ser Leu Arg Arg Gln Glu Leu Ala Arg Ile Ala
 690 695 700
 Ser Ala Asp Leu Leu Asn Met Leu Thr Val Gln Glu Val Cys Gln Ser
 705 710 715 720
 Leu Ser Leu Val Trp Asp Ala Val Leu Asp Ala Ala Leu Asp Ala Glu
 725 730 735
 Ile Arg Ala Ala Leu Asn Asp Pro Gln Lys Pro Asp Gln Pro Leu Ala
 740 745 750
 Asn Ile Ser Val Ile Gly Met Gly Arg Leu Gly Gly Ala Glu Leu Gly
 755 760 765
 Tyr Gly Ser Asp Ala Asp Val Met Phe Val Cys Glu Pro Val Ala Gly
 770 775 780
 Val Glu Glu His Glu Ala Val Thr Trp Ser Ile Ala Ile Cys Asp Ser
 785 790 795 800
 Met Arg Ser Arg Leu Ala Gln Pro Ser Gly Asp Pro Pro Leu Glu Val
 805 810 815
 Asp Leu Gly Leu Arg Pro Glu Gly Arg Ser Gly Ala Ile Val Arg Thr
 820 825 830
 Val Asp Ser Tyr Val Lys Tyr Tyr Glu Lys Trp Gly Glu Thr Trp Glu
 835 840 845
 Ile Gln Ala Leu Leu Arg Ala Ala Trp Val Ala Gly Asp Arg Glu Leu
 850 855 860
 Gly Ile Lys Phe Leu Glu Ser Ile Asp Arg Phe Arg Tyr Pro Val Asp

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865	870	875	880
Gly Ala Thr Gln Ala Gln Leu Arg Glu Val Arg Arg Ile Lys Ala Arg			
885	890	895	
Val Asp Asn Glu Arg Leu Pro Arg Gly Ala Asp Arg Asn Thr His Thr			
900	905	910	
Lys Leu Gly Arg Gly Ala Leu Thr Asp Ile Glu Trp Thr Val Gln Leu			
915	920	925	
Leu Thr Met Met His Ala His Glu Ile Pro Glu Leu His Asn Thr Ser			
930	935	940	
Thr Leu Glu Val Leu Glu Val Leu Glu Lys His Gln Ile Ile Asn Pro			
945	950	955	960
Val Gln Val Gln Thr Leu Arg Glu Ala Trp Leu Thr Ala Thr Ala Ala			
965	970	975	
Arg Asn Ala Leu Val Leu Val Arg Gly Lys Arg Leu Asp Gln Leu Pro			
980	985	990	
Thr Pro Gly Pro His Leu Ala Gln Val Ala Gly Ala Ser Gly Trp Asp			
995	1000	1005	
Pro Asn Glu Tyr Gln Glu Tyr Leu Glu Asn Tyr Leu Lys Val Thr Arg			
1010	1015	1020	
Lys Ser Arg Gln Val Val Asp Glu Val Phe Trp Gly Val Asp Ser Met			
025	1030	1035	1040
Glu Gln Arg Glu Phe			
1045			

<210> 19
<211> 1434
<212> DNA
<213> *Brevibacterium lactofermentum*

<220>
<221> CDS
<222> (1)..(1434)

<400> 19

gtg gcg ttt gaa acc ccg gaa gaa att gtc aag ttc atc aag gat gaa	48
Val Ala Phe Glu Thr Pro Glu Glu Ile Val Lys Phe Ile Lys Asp Glu	
1 5 10 15	
aac gtc gag ttc gtt gac gtt cga ttc acc gac ctt ccc ggc acc gag	96
Asn Val Glu Phe Val Asp Val Arg Phe Thr Asp Leu Pro Gly Thr Glu	
20 25 30	
cag cac ttc agc atc cca gct gcc agc ttc gat gca gat aca gtc gaa	144
Gln His Phe Ser Ile Pro Ala Ala Ser Phe Asp Ala Asp Thr Val Glu	
35 40 45	
gaa ggt ctc gca ttc gac gga tcc tcg atc cgt ggc ttc acc acg atc	192
Glu Gly Leu Ala Phe Asp Gly Ser Ser Ile Arg Gly Phe Thr Thr Ile	
50 55 60	
gac gaa tct gac atg aat ctc ctg cca gac ctc gga acg gcc acc ctt	240
Asp Glu Ser Asp Met Asn Leu Leu Pro Asp Leu Gly Thr Ala Thr Leu	
65 70 75 80	
gat cca ttc cgc aag gca aag acc ctg aac gtt aag ttc ttc gtt cac	288
Asp Pro Phe Arg Lys Ala Lys Thr Leu Asn Val Lys Phe Phe Val His	
85 90 95	
gat cct ttc acc cgc gag gca ttc tcc cgc gac cca cgc aac gta gca	336
Asp Pro Phe Thr Arg Glu Ala Phe Ser Arg Asp Pro Arg Asn Val Ala	
100 105 110	
cgc aag gca gag cag tac ctg gca tcc acc ggc att gca gac acc tgc	384
Arg Lys Ala Glu Gln Tyr Leu Ala Ser Thr Gly Ile Ala Asp Thr Cys	
115 120 125	
aac ttc ggc gcc gag gct gag ttc tac ctc ttc gac tcc gtt cgc tac	432
Asn Phe Glu Ala Glu Ala Glu Phe Tyr Leu Phe Asp Ser Val Arg Tyr	
130 135 140	
tcc acc gag atg aac tcc ggc ttc tac gaa gta gat acc gaa gaa ggc	480
Ser Thr Glu Met Asn Ser Gly Phe Tyr Glu Val Asp Thr Glu Glu Gly	

OP1741seqUS

145	150	155	160	
tgg tgg aac cgt ggc aag gaa acc aac	Trp Trp Asn Arg Gly Lys Glu Thr Asn	ctc gac gga acc cca aac ctg	Leu Asp Gly Thr Pro Asn Leu	528
165	165	170	175	
ggc gca aag aac cgc gtc aag ggt ggc tac ttc cca gta gca cca tac	Gly Ala Lys Asn Arg Val Lys Gly Tyr Phe Pro Val Ala Pro Tyr	180 185	190	576
gac caa acc gtt gac gtg cgc gat gac atg gtt cgc aac ctc gca gct	Asp Gln Thr Val Asp Val Arg Asp Asp Met Val Arg Asn Leu Ala Ala	195 200	205	624
tcc ggc ttc gct ctt gag cgt ttc cac cac gaa gtc ggt ggc gga cag	Ser Gly Phe Ala Leu Glu Arg Phe His His Glu Val Gly Gly Gln	210 215	220	672
cag gaa atc aac tac cgc ttc aac acc atg ctc cac gcg gca gat gat	Gln Glu Ile Asn Tyr Arg Phe Asn Thr Met Leu His Ala Ala Asp Asp	225 230	235 240	720
atc cag acc ttc aag tac atc atc aag aac acc gct cgc ctc cac ggc	Ile Gln Thr Phe Lys Tyr Ile Lys Asn Thr Ala Arg Leu His Gly	245	250 255	768
aag gct gca acc ttc atg cct aag cca ctg gct ggc gac aac ggt tcc	Lys Ala Ala Thr Phe Met Pro Lys Pro Leu Ala Gly Asp Asn Gly Ser	260	265 270	816
ggc atg cac gct cac cag tcc ctc tgg aag gac ggc aag cca ctc ttc	Gly Met His Ala His Gln Ser Leu Trp Lys Asp Gly Lys Pro Leu Phe	275 280	285	864
cac gat gag tcc ggc tac gca ggc ctg tcc gac atc gcc cgc tac tac	His Asp Glu Ser Gly Tyr Ala Gly Leu Ser Asp Ile Ala Arg Tyr Tyr	290 295	300	912
atc ggc ggc atc ctg cac cac gca ggc gct gtt ctg gcg ttc acc aac	Ile Gly Gly Ile Leu His His Ala Gly Ala Val Leu Ala Phe Thr Asn	305 310	315 320	960
gca acc ctg aac tcc tac cac cgt ctg gtt cca ggc ttc gag gct cca	Ala Thr Leu Asn Ser Tyr His Arg Leu Val Pro Gly Phe Glu Ala Pro	325	330 335	1008
atc aac ctg gtg tac tca cag cgc aac cgt tcc gct gct gtc cgt atc	Ile Asn Leu Val Tyr Ser Gln Arg Asn Arg Ser Ala Ala Val Arg Ile	340	345 350	1056
cca atc acc gga tcc aac cca aag gca aag cgc atc gaa ttc cgc gct	Pro Ile Thr Gly Ser Asn Pro Lys Ala Lys Arg Ile Glu Phe Arg Ala	355	360 365	1104
cca gac cca tca ggc aac cca tac ctg ggc ttc gca gcg atg atg atg	Pro Asp Pro Ser Gly Asn Pro Tyr Leu Gly Phe Ala Ala Met Met Met	370	375 380	1152
gcc ggc ctc gac ggc atc aag aac cgc atc gag cca cac gct cca gtg	Ala Gly Leu Asp Gly Ile Lys Asn Arg Ile Glu Pro His Ala Pro Val	385 390	395 400	1200
gac aag gac ctc tac gaa ctg cca cca gag gaa gct gca tcc att cca	Asp Lys Asp Leu Tyr Glu Leu Pro Pro Glu Glu Ala Ala Ser Ile Pro	405	410 415	1248
cag gca cca acc tcc ctg gaa gca tcc ctg aag gca ctg cag gaa gac	Gln Ala Pro Thr Ser Leu Glu Ala Ser Leu Lys Ala Leu Gln Glu Asp	420	425 430	1296
acc gac ttc ctc acc gag tct gac gtc ttc acc gag gat ctc atc gag	Thr Asp Phe Leu Thr Glu Ser Asp Val Phe Thr Glu Asp Leu Ile Glu	435	440 445	1344
gcg tac atc cag tac aag tac gac aac gag atc tcc cca gtt cgc ctg	Ala Tyr Ile Gln Tyr Lys Tyr Asp Asn Glu Ile Ser Pro Val Arg Leu	450 455	460	1392
cgc cca acc ccg cag gaa ttc gaa ttg tac ttc gac tgc taa	Arg Pro Thr Pro Gln Glu Phe Glu Leu Tyr Phe Asp Cys	465 470	475	1434

OP1741seqUS

<211> 477

<212> PRT

<213> Brevibacterium lactofermentum

<400> 20

Val Ala Phe Glu Thr Pro Glu Glu Ile Val Lys Phe Ile Lys Asp Glu
 1 5 10 15
 Asn Val Glu Phe Val Asp Val Arg Phe Thr Asp Leu Pro Gly Thr Glu
 20 25 30
 Gln His Phe Ser Ile Pro Ala Ala Ser Phe Asp Ala Asp Thr Val Glu
 35 40 45
 Glu Gly Leu Ala Phe Asp Gly Ser Ser Ile Arg Gly Phe Thr Thr Ile
 50 55 60
 Asp Glu Ser Asp Met Asn Leu Leu Pro Asp Leu Gly Thr Ala Thr Leu
 65 70 75 80
 Asp Pro Phe Arg Lys Ala Lys Thr Leu Asn Val Lys Phe Phe Val His
 85 90 95
 Asp Pro Phe Thr Arg Glu Ala Phe Ser Arg Asp Pro Arg Asn Val Ala
 100 105 110
 Arg Lys Ala Glu Gln Tyr Leu Ala Ser Thr Gly Ile Ala Asp Thr Cys
 115 120 125
 Asn Phe Gly Ala Glu Ala Glu Phe Tyr Leu Phe Asp Ser Val Arg Tyr
 130 135 140
 Ser Thr Glu Met Asn Ser Gly Phe Tyr Glu Val Asp Thr Glu Glu Gly
 145 150 155 160
 Trp Trp Asn Arg Gly Lys Glu Thr Asn Leu Asp Gly Thr Pro Asn Leu
 165 170 175
 Gly Ala Lys Asn Arg Val Lys Gly Gly Tyr Phe Pro Val Ala Pro Tyr
 180 185 190
 Asp Gln Thr Val Asp Val Arg Asp Asp Met Val Arg Asn Leu Ala Ala
 195 200 205
 Ser Gly Phe Ala Leu Glu Arg Phe His His Glu Val Gly Gly Gly Gln
 210 215 220
 Gln Glu Ile Asn Tyr Arg Phe Asn Thr Met Leu His Ala Ala Asp Asp
 225 230 235 240
 Ile Gln Thr Phe Lys Tyr Ile Ile Lys Asn Thr Ala Arg Leu His Gly
 245 250 255
 Lys Ala Ala Thr Phe Met Pro Lys Pro Leu Ala Gly Asp Asn Gly Ser
 260 265 270
 Gly Met His Ala His Gln Ser Leu Trp Lys Asp Gly Lys Pro Leu Phe
 275 280 285
 His Asp Glu Ser Gly Tyr Ala Gly Leu Ser Asp Ile Ala Arg Tyr Tyr
 290 295 300
 Ile Gly Gly Ile Leu His His Ala Gly Ala Val Leu Ala Phe Thr Asn
 305 310 315 320
 Ala Thr Leu Asn Ser Tyr His Arg Leu Val Pro Gly Phe Glu Ala Pro
 325 330 335
 Ile Asn Leu Val Tyr Ser Gln Arg Asn Arg Ser Ala Ala Val Arg Ile
 340 345 350
 Pro Ile Thr Gly Ser Asn Pro Lys Ala Lys Arg Ile Glu Phe Arg Ala
 355 360 365
 Pro Asp Pro Ser Gly Asn Pro Tyr Leu Gly Phe Ala Ala Met Met Met
 370 375 380
 Ala Gly Leu Asp Gly Ile Lys Asn Arg Ile Glu Pro His Ala Pro Val
 385 390 395 400
 Asp Lys Asp Leu Tyr Glu Leu Pro Pro Glu Glu Ala Ala Ser Ile Pro
 405 410 415
 Gln Ala Pro Thr Ser Leu Glu Ala Ser Leu Lys Ala Leu Gln Glu Asp
 420 425 430
 Thr Asp Phe Leu Thr Glu Ser Asp Val Phe Thr Glu Asp Leu Ile Glu
 435 440 445
 Ala Tyr Ile Gln Tyr Lys Tyr Asp Asn Glu Ile Ser Pro Val Arg Leu
 450 455 460

OP1741seqUS

Arg	Pro	Thr	Pro	Gln	Glu	Phe	Glu	Leu	Tyr	Phe	Asp	Cys	
465				470					475				

<210> 21
<211> 672
<212> DNA
<213> *Brevibacterium lactofermentum*

<220>
<221> CDS
<222> (1)..(669)

<400> 21

atg	gca	gga	gca	gtg	gga	cgc	ccc	cg	aga	tca	gct	ccg	cga	cg	gca	48
Met	Ala	Gly	Ala	Val	Gly	Arg	Pro	Arg	Arg	Ser	Ala	Pro	Arg	Arg	Ala	
1				5				10						15		
ggc	aag	aat	cct	cgc	gag	gag	att	ctt	gac	gcc	tct	gct	gag	ctt	ttc	96
Gly	Lys	Asn	Pro	Arg	Glu	Glu	Ile	Leu	Asp	Ala	Ser	Ala	Glu	Leu	Phe	
							20			25			30			
acc	cat	caa	ggc	ttc	gca	aca	acc	tcc	acg	cat	caa	atc	gct	gat	gcc	144
Thr	His	Gln	Gly	Phe	Ala	Thr	Thr	Ser	Thr	His	Gln	Ile	Ala	Asp	Ala	
							35			40			45			
gtg	gga	atc	cgc	caa	gcc	tcg	ctg	tat	tat	cac	ttc	ccg	tct	aag	acg	192
Val	Gly	Ile	Arg	Gln	Ala	Ser	Leu	Tyr	Tyr	His	Phe	Pro	Ser	Lys	Thr	
							50			55			60			
gaa	atc	ttc	ctc	acc	ctc	ctg	aaa	tct	acc	gtc	gag	ccg	tcc	act	gtg	240
Glu	Ile	Phe	Leu	Thr	Leu	Lys	Ser	Thr	Val	Glu	Pro	Ser	Thr	Val		
							65			70			75			80
ctc	gcc	gaa	gac	tta	agc	atc	ctg	gat	gca	gga	cct	gag	atg	cgc	ctc	288
Leu	Ala	Glu	Asp	Leu	Ser	Ile	Leu	Asp	Ala	Gly	Pro	Glu	Met	Arg	Leu	
							85			90			95			
tgg	gca	atc	gtt	gcc	tcc	gaa	gtg	cgt	ctg	ctg	ctg	tcc	acc	aag	tgg	336
Trp	Ala	Ile	Val	Ala	Ser	Glu	Val	Arg	Leu	Leu	Leu	Ser	Thr	Lys	Trp	
							100			105			110			
aac	gtc	ggt	cgc	ctg	tac	caa	ctc	ccc	atc	gtt	ggt	tct	gaa	gag	ttc	384
Asn	Val	Gly	Arg	Leu	Tyr	Gln	Leu	Pro	Ile	Val	Gly	Ser	Glu	Glu	Phe	
							115			120			125			
gcc	gag	tac	cac	agc	cag	cgc	gaa	gcc	ctc	acc	aac	atc	ttc	cgc	gac	432
Ala	Glu	Tyr	His	Ser	Gln	Arg	Glu	Ala	Leu	Thr	Asn	Ile	Phe	Arg	Asp	
							130			135			140			
ctc	gcc	acc	gaa	atc	gtc	ggt	gac	gac	ccc	cgc	gca	gaa	ctc	ccc	ttc	480
Leu	Ala	Thr	Glu	Ile	Val	Gly	Asp	Asp	Pro	Arg	Ala	Glu	Leu	Pro	Phe	
							145			150			155			160
cac	atc	acc	atg	tcg	gtg	atc	gaa	atg	cgt	cgc	aac	gac	ggc	aag	att	528
His	Ile	Thr	Met	Ser	Val	Ile	Glu	Met	Arg	Arg	Asn	Asp	Gly	Lys	Ile	
							165			170			175			
cca	agc	ccg	ctt	tcc	gca	gac	agc	ctc	ccg	gag	acc	gca	att	atg	ctt	576
Pro	Ser	Pro	Leu	Ser	Ala	Asp	Ser	Leu	Pro	Glu	Thr	Ala	Ile	Met	Leu	
							180			185			190			
gcc	gac	gcc	tcc	ctc	gcc	gtc	ctc	ggc	gct	tcg	ctg	ccc	gcc	gac	cg	624
Ala	Asp	Ala	Ser	Leu	Ala	Val	Leu	Gly	Ala	Ser	Leu	Pro	Ala	Asp	Arg	
							195			200			205			
gtc	gaa	aaa	acg	ctt	gaa	cta	atc	aag	cag	gct	gac	gct	aaa	taa	cca	672
Val	Glu	Lys	Thr	Leu	Glu	Leu	Ile	Lys	Gln	Ala	Asp	Ala	Lys			
							210			215			220			

<210> 22
<211> 222
<212> PRT
<213> *Brevibacterium lactofermentum*

<400> 22
Met Ala Gly Ala Val Gly Arg Pro Arg Arg Ser Ala Pro Arg Arg Ala

OP1741seqUS

1	5	10	15												
Gly	Lys	Asn	Pro	Arg	Glu	Glu	Ile	Leu	Asp	Ala	Ser	Ala	Glu	Leu	Phe
20	25	30													
Thr	His	Gln	Gly	Phe	Ala	Thr	Thr	Ser	Thr	His	Gln	Ile	Ala	Asp	Ala
35	40	45													
Val	Gly	Ile	Arg	Gln	Ala	Ser	Leu	Tyr	Tyr	His	Phe	Pro	Ser	Lys	Thr
50	55	60													
Glu	Ile	Phe	Leu	Thr	Leu	Leu	Lys	Ser	Thr	Val	Glu	Pro	Ser	Thr	Val
65	70	75	80												
Leu	Ala	Glu	Asp	Leu	Ser	Ile	Leu	Asp	Ala	Gly	Pro	Glu	Met	Arg	Leu
85	90	95													
Trp	Ala	Ile	Val	Ala	Ser	Glu	Val	Arg	Leu	Leu	Leu	Ser	Thr	Lys	Trp
100	105	110													
Asn	Val	Gly	Arg	Leu	Tyr	Gln	Leu	Pro	Ile	Val	Gly	Ser	Glu	Glu	Phe
115	120	125													
Ala	Glu	Tyr	His	Ser	Gln	Arg	Glu	Ala	Leu	Thr	Asn	Ile	Phe	Arg	Asp
130	135	140													
Leu	Ala	Thr	Glu	Ile	Val	Gly	Asp	Asp	Pro	Arg	Ala	Glu	Leu	Pro	Phe
145	150	155	160												
His	Ile	Thr	Met	Ser	Val	Ile	Glu	Met	Arg	Arg	Asn	Asp	Gly	Lys	Ile
165	170	175													
Pro	Ser	Pro	Leu	Ser	Ala	Asp	Ser	Leu	Pro	Glu	Thr	Ala	Ile	Met	Leu
180	185	190													
Ala	Asp	Ala	Ser	Leu	Ala	Val	Leu	Gly	Ala	Ser	Leu	Pro	Ala	Asp	Arg
195	200	205													
Val	Glu	Lys	Thr	Leu	Glu	Leu	Ile	Lys	Gln	Ala	Asp	Ala	Lys		
210	215	220													

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<211> 2076
<212> DNA
<213> *Brevibacterium lactofermentum*

<220>
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Met	Asn	Asn	Pro	Ala	Gln	Leu	Arg	Gln	Asp	Thr	Glu	Lys	Glu	Val	Leu
1	5	10	15												
gcg	ttg	ctg	ggc	tct	ttg	gtt	tta	ccc	gcc	acc	gca	ctt	gcc	gcc	96
Ala	Leu	Leu	Gly	Ser	Leu	Val	Leu	Pro	Ala	Gly	Thr	Ala	Leu	Ala	Ala
20	25	30													
acc	gga	tct	ttg	gcc	agg	tcc	gaa	ctc	acg	ccg	tat	tcc	gat	ttg	gac
Thr	Gly	Ser	Leu	Ala	Arg	Ser	Glu	Leu	Thr	Pro	Tyr	Ser	Asp	Leu	Asp
35	40	45													
ctc	att	ttg	atc	cat	cca	cca	ggg	gca	acc	ccg	gat	ggc	gtg	gag	gat
Leu	Ile	Leu	Ile	His	Pro	Pro	Gly	Ala	Thr	Pro	Asp	Gly	Val	Glu	Asp
50	55	60													
ttg	tgg	tac	ccg	att	tgg	gac	gca	aaa	aag	cgc	ctc	gac	tac	tcc	gtg
Leu	Trp	Tyr	Pro	Ile	Trp	Asp	Ala	Lys	Lys	Arg	Leu	Asp	Tyr	Ser	Val
65	70	75	80												
cgc	acc	cca	gat	gag	tgc	gtg	gct	atg	att	tct	gca	gat	tcc	act	gca
Arg	Thr	Pro	Asp	Glu	Cys	Val	Ala	Met	Ile	Ser	Ala	Asp	Ser	Thr	Ala
85	90	95													
gcc	ctt	gcc	atg	ctt	gac	ctg	cga	ttt	att	gct	ggc	gat	gag	gat	ctg
Ala	Leu	Ala	Met	Leu	Asp	Leu	Arg	Phe	Ile	Ala	Gly	Asp	Glu	Asp	Leu
100	105	110													
tgt	gcc	aaa	acg	cgc	cg	atc	gtg	gag	aag	tgg	cgc	cag	gaa	ctc	
Cys	Ala	Lys	Thr	Arg	Arg	Arg	Ile	Val	Glu	Lys	Trp	Arg	Gln	Glu	Leu
115	120	125													
aac	aaa	aac	ttc	gac	gcc	gtt	gtg	gac	acc	gca	att	gcc	cgt	tgg	cgc

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Asn	Lys	Asn	Phe	Asp	Ala	Val	Val	Asp	Thr	Ala	Ile	Ala	Arg	Trp	Arg	
130						135					140					
cgc	tcc	gga	ccc	gtc	gtg	gca	atg	acg	cg	cca	gat	ctt	aaa	cac	ggc	480
Arg	Ser	Gly	Pro	Val	Val	Ala	Met	Thr	Arg	Pro	Asp	Leu	Lys	His	Gly	
145						150					155					160
agg	gga	ggg	ctg	cgc	gat	tcc	gaa	ctg	atc	aag	gcc	ctc	gcg	ctc	ggc	528
Arg	Gly	Gly	Leu	Arg	Asp	Phe	Glu	Leu	Ile	Lys	Ala	Leu	Ala	Leu	Gly	
						165				170					175	
cac	cta	tgc	aac	gtt	cca	cag	cta	gat	acg	caa	cac	cag	ctg	ctt	ctc	576
His	Leu	Cys	Asn	Val	Pro	Gln	Leu	Asp	Thr	Gln	His	Gln	Leu	Leu	Leu	
						180				185					190	
gac	gcc	cgc	acc	ttg	ctg	cac	gtc	cac	gcg	cga	cgc	tcc	cgc	gac	gtc	624
Asp	Ala	Arg	Thr	Leu	Leu	His	Val	His	Ala	Arg	Arg	Ser	Arg	Asp	Val	
						195				200					205	
ctt	gat	ccc	gaa	ttt	gcf	gtg	gat	gtg	gcc	atg	gat	ttg	ggc	ttt	gtt	672
Leu	Asp	Pro	Glu	Phe	Ala	Val	Asp	Val	Ala	Met	Asp	Leu	Gly	Phe	Val	
						210				215					220	
gac	cgc	tat	cac	tta	ggc	cgg	gag	atc	gcc	gat	gca	gcc	cgc	gcc	att	720
Asp	Arg	Tyr	His	Leu	Gly	Arg	Glu	Ile	Ala	Asp	Ala	Ala	Arg	Ala	Ile	
						225				230					235	240
gat	gac	ggc	ctg	acc	acc	gcf	ctg	gcc	acc	gcc	cgt	ggc	att	ttg	cca	768
Asp	Asp	Gly	Leu	Thr	Thr	Ala	Leu	Ala	Thr	Ala	Arg	Gly	Ile	Leu	Pro	
						245				250					255	
cgt	cgc	acg	ggt	ttt	gct	ttt	agg	aat	gct	tct	cga	cgc	cca	ctt	gat	816
Arg	Arg	Thr	Gly	Phe	Ala	Phe	Arg	Asn	Ala	Ser	Arg	Arg	Pro	Leu	Asp	
						260				265					270	
ctt	gat	gtc	gtc	gac	gcc	aac	ggc	act	atc	gaa	ttg	tcc	aaa	aaa	cca	864
Leu	Asp	Val	Val	Asp	Ala	Asn	Gly	Thr	Ile	Glu	Leu	Ser	Lys	Lys	Pro	
						275				280					285	
gat	ctt	aat	gat	ccc	gca	ctt	cca	ctt	cga	gtg	gcc	gca	gcc	gca	gcf	912
Asp	Leu	Asn	Asp	Pro	Ala	Leu	Pro	Leu	Arg	Val	Ala	Ala	Ala	Ala	Ala	
						290				295					300	
acc	acc	gga	ctt	ccg	gtg	gca	gaa	tca	acc	tgg	gct	cga	ctt	aat	gaa	960
Thr	Thr	Gly	Leu	Pro	Val	Ala	Glu	Ser	Thr	Trp	Ala	Arg	Leu	Asn	Glu	
						305				310					315	320
tgc	ccg	cca	ctt	cct	gag	cca	tgg	cct	gcc	aat	gca	gca	ggg	gac	ttc	1008
Cys	Pro	Pro	Leu	Pro	Glu	Pro	Trp	Pro	Ala	Asn	Ala	Ala	Gly	Asp	Phe	
						325				330					335	
ttt	cg	att	ctc	tcc	agt	ccg	aaa	aac	tca	cgc	cga	gtg	gtg	aaa	aat	1056
Phe	Arg	Ile	Leu	Ser	Ser	Pro	Lys	Asn	Ser	Arg	Arg	Val	Val	Lys	Asn	
						340				345					350	
atg	gat	cgc	cac	gga	ttg	tgg	tcg	cgt	ttt	gtt	cca	gaa	tgg	gac	cgc	1104
Met	Asp	Arg	His	Gly	Leu	Trp	Ser	Arg	Phe	Val	Pro	Glu	Trp	Asp	Arg	
						355				360					365	
atc	aaa	ggg	ctt	atg	ccc	cgt	gaa	ccc	agc	cat	att	tcc	acc	atc	gat	1152
Ile	Lys	Gly	Leu	Met	Pro	Arg	Glu	Pro	Ser	His	Ile	Ser	Thr	Ile	Asp	
						370				375					380	
gaa	cat	agt	ctg	aac	act	gtt	gca	gga	tgt	gcf	cta	gaa	act	gtg	acc	1200
Glu	His	Ser	Leu	Asn	Thr	Val	Ala	Gly	Cys	Ala	Leu	Glu	Thr	Val	Thr	
						385				390					395	400
gtc	gcf	cgc	ccc	gat	ctt	tta	gtt	tgg	gga	gcc	ttg	tac	cac	gac	att	1248
Val	Ala	Arg	Pro	Asp	Leu	Leu	Val	Leu	Gly	Ala	Leu	Tyr	His	Asp	Ile	
						405				410					415	
ggc	aag	ggc	tcc	ccg	cgt	cca	cac	gaa	caa	gta	ggt	gca	gag	atg	gtg	1296
Gly	Lys	Gly	Phe	Pro	Arg	Pro	His	Glu	Gln	Val	Gly	Ala	Glu	Met	Val	
						420				425					430	
gcf	agg	gcc	gcf	agc	cgc	atg	ggg	ttg	aac	ctt	cgc	gat	cgt	gcc	agc	1344
Ala	Arg	Ala	Ala	Ser	Arg	Met	Gly	Leu	Asn	Leu	Arg	Asp	Arg	Ala	Ser	
						435				440					445	
gtg	caa	acg	ctg	gtc	gcc	gag	cac	acc	gcf	gtg	gcc	aaa	atc	gcc	gcf	1392
Val	Gln	Thr	Leu	Val	Ala	Glu	His	Thr	Ala	Val	Ala	Lys	Ile	Ala	Ala	
						450				455					460	
gcf	ctt	gat	ccc	tcc	tcg	gag	ggc	gcc	gtc	gat	aag	ctg	ctt	gat	gct	1440

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Arg	Leu	Asp	Pro	Ser	Ser	Glu	Gly	Ala	Val	Asp	Lys	Leu	Leu	Asp	Ala	
465						470				475					480	
gtt	agg	tat	gac	ctg	gtg	aca	ttg	aat	ctg	ctt	gag	gtg	cta	aca	gaa	1488
Val	Arg	Tyr	Asp	Leu	Val	Thr	Leu	Asn	Leu	Leu	Glu	Val	Leu	Thr	Glu	
									485	490				495		
gct	gat	gcg	aaa	gcc	acg	ggg	cct	ggc	gta	tgg	acg	gcg	cgt	ttg	gag	1536
Ala	Asp	Ala	Lys	Ala	Thr	Gly	Pro	Gly	Val	Trp	Thr	Ala	Arg	Leu	Glu	
									500	505			510			
cat	gcg	ctg	cgg	att	gtg	tgc	aag	cgt	gcf	cgt	gat	cgc	ctc	acc	gat	1584
His	Ala	Leu	Arg	Ile	Val	Cys	Lys	Arg	Ala	Arg	Asp	Arg	Leu	Thr	Asp	
									515	520		525				
att	cgc	ccg	gtt	gcf	ccg	atg	att	gcf	ccg	cgt	agc	gaa	att	ggt	ttg	1632
Ile	Arg	Pro	Val	Ala	Pro	Met	Ile	Ala	Pro	Arg	Ser	Glu	Ile	Gly	Leu	
									530	535		540				
gtg	gaa	cgc	gat	ggc	gtg	ttc	aca	gtg	caa	tgg	cac	ggc	gaa	gac	tta	1680
Val	Glu	Arg	Asp	Gly	Val	Phe	Thr	Val	Gln	Trp	His	Gly	Glu	Asp	Leu	
									545	550		555			560	
cat	cgg	att	ctt	ggc	gta	att	tat	gcc	aaa	gga	tgg	aca	atc	acc	gcf	1728
His	Arg	Ile	Leu	Gly	Val	Ile	Tyr	Ala	Lys	Gly	Trp	Thr	Ile	Thr	Ala	
									565	570		575				
gcf	cgc	atg	ctg	gcc	aat	ggt	caa	tgg	agt	gcf	gaa	ttt	gat	gtc	cgc	1776
Ala	Arg	Met	Leu	Ala	Asn	Gly	Gln	Trp	Ser	Ala	Glu	Phe	Asp	Val	Arg	
									580	585		590				
gca	aac	ggc	ccc	caa	gat	ttt	gat	ccg	cag	cat	ttc	ctg	cag	gca	tat	1824
Ala	Asn	Gly	Pro	Gln	Asp	Phe	Asp	Pro	Gln	His	Phe	Leu	Gln	Ala	Tyr	
									595	600		605				
caa	tcc	ggf	gtg	ttt	tcc	gag	gtt	ccc	att	cca	gca	cct	ggg	ata	aca	1872
Gln	Ser	Gly	Val	Phe	Ser	Glu	Val	Pro	Ile	Pro	Ala	Pro	Gly	Ile	Thr	
									610	615		620				
gcc	aca	ttt	tgg	cac	ggg	aac	act	tta	gaa	gtg	cgc	act	gag	ctt	cgc	1920
Ala	Thr	Phe	Trp	His	Gly	Asn	Thr	Leu	Glu	Val	Arg	Thr	Glu	Leu	Arg	
									625	630		635			640	
aca	gga	gct	att	ttt	gcc	ctg	ctc	aga	aca	ttg	ccc	gat	gcc	ctc	tgg	1968
Thr	Gly	Ala	Ile	Phe	Ala	Leu	Leu	Arg	Thr	Leu	Pro	Asp	Ala	Leu	Trp	
									645	650		655				
atc	aac	gct	gtg	acc	cgc	ggt	gcf	acc	ctg	att	atc	cag	gca	gca	ctg	2016
Ile	Asn	Ala	Val	Thr	Arg	Gly	Ala	Thr	Leu	Ile	Ile	Gln	Ala	Ala	Leu	
									660	665		670				
aag	ccc	ggc	tcc	gat	cga	gca	acg	gtg	gaa	cgc	tcc	gta	gtc	agg	tcg	2064
Lys	Pro	Gly	Phe	Asp	Arg	Ala	Thr	Val	Glu	Arg	Ser	Val	Val	Arg	Ser	
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ttg	gca	ggt	agc													2076
Leu	Ala	Gly	Ser													
									690							

<210> 24

<211> 692

<212> PRT

<213> Brevibacterium lactofermentum

<400> 24

Met	Asn	Asn	Pro	Ala	Gln	Leu	Arg	Gln	Asp	Thr	Glu	Lys	Glu	Val	Leu	
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Ala	Leu	Leu	Gly	Ser	Leu	Val	Leu	Pro	Ala	Gly	Thr	Ala	Leu	Ala		
									20	25		30				
Thr	Gly	Ser	Leu	Ala	Arg	Ser	Glu	Leu	Thr	Pro	Tyr	Ser	Asp	Leu	Asp	
									35	40		45				
Leu	Ile	Leu	Ile	His	Pro	Pro	Gly	Ala	Thr	Pro	Asp	Gly	Val	Glu	Asp	
									50	55		60				
Leu	Trp	Tyr	Pro	Ile	Trp	Asp	Ala	Lys	Lys	Arg	Leu	Asp	Tyr	Ser	Val	
									65	70		75			80	
Arg	Thr	Pro	Asp	Glu	Cys	Val	Ala	Met	Ile	Ser	Ala	Asp	Ser	Thr	Ala	
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Ala Leu Ala Met Leu Asp Leu Arg Phe Ile Ala Gly Asp Glu Asp Leu
 100 105 110
 Cys Ala Lys Thr Arg Arg Arg Ile Val Glu Lys Trp Arg Gln Glu Leu
 115 120 125
 Asn Lys Asn Phe Asp Ala Val Val Asp Thr Ala Ile Ala Arg Trp Arg
 130 135 140
 Arg Ser Gly Pro Val Val Ala Met Thr Arg Pro Asp Leu Lys His Gly
 145 150 155 160
 Arg Gly Gly Leu Arg Asp Phe Glu Leu Ile Lys Ala Leu Ala Leu Gly
 165 170 175
 His Leu Cys Asn Val Pro Gln Leu Asp Thr Gln His Gln Leu Leu Leu
 180 185 190
 Asp Ala Arg Thr Leu Leu His Val His Ala Arg Arg Ser Arg Asp Val
 195 200 205
 Leu Asp Pro Glu Phe Ala Val Asp Val Ala Met Asp Leu Gly Phe Val
 210 215 220
 Asp Arg Tyr His Leu Gly Arg Glu Ile Ala Asp Ala Ala Arg Ala Ile
 225 230 235 240
 Asp Asp Gly Leu Thr Thr Ala Leu Ala Thr Ala Arg Gly Ile Leu Pro
 245 250 255
 Arg Arg Thr Gly Phe Ala Phe Arg Asn Ala Ser Arg Arg Pro Leu Asp
 260 265 270
 Leu Asp Val Val Asp Ala Asn Gly Thr Ile Glu Leu Ser Lys Lys Pro
 275 280 285
 Asp Leu Asn Asp Pro Ala Leu Pro Leu Arg Val Ala Ala Ala Ala Ala
 290 295 300
 Thr Thr Gly Leu Pro Val Ala Glu Ser Thr Trp Ala Arg Leu Asn Glu
 305 310 315 320
 Cys Pro Pro Leu Pro Glu Pro Trp Pro Ala Asn Ala Ala Gly Asp Phe
 325 330 335
 Phe Arg Ile Leu Ser Ser Pro Lys Asn Ser Arg Arg Val Val Lys Asn
 340 345 350
 Met Asp Arg His Gly Leu Trp Ser Arg Phe Val Pro Glu Trp Asp Arg
 355 360 365
 Ile Lys Gly Leu Met Pro Arg Glu Pro Ser His Ile Ser Thr Ile Asp
 370 375 380
 Glu His Ser Leu Asn Thr Val Ala Gly Cys Ala Leu Glu Thr Val Thr
 385 390 395 400
 Val Ala Arg Pro Asp Leu Leu Val Leu Gly Ala Leu Tyr His Asp Ile
 405 410 415
 Gly Lys Gly Phe Pro Arg Pro His Glu Gln Val Gly Ala Glu Met Val
 420 425 430
 Ala Arg Ala Ala Ser Arg Met Gly Leu Asn Leu Arg Asp Arg Ala Ser
 435 440 445
 Val Gln Thr Leu Val Ala Glu His Thr Ala Val Ala Lys Ile Ala Ala
 450 455 460
 Arg Leu Asp Pro Ser Ser Glu Gly Ala Val Asp Lys Leu Leu Asp Ala
 465 470 475 480
 Val Arg Tyr Asp Leu Val Thr Leu Asn Leu Leu Glu Val Leu Thr Glu
 485 490 495
 Ala Asp Ala Lys Ala Thr Gly Pro Gly Val Trp Thr Ala Arg Leu Glu
 500 505 510
 His Ala Leu Arg Ile Val Cys Lys Arg Ala Arg Asp Arg Leu Thr Asp
 515 520 525
 Ile Arg Pro Val Ala Pro Met Ile Ala Pro Arg Ser Glu Ile Gly Leu
 530 535 540
 Val Glu Arg Asp Gly Val Phe Thr Val Gln Trp His Gly Glu Asp Leu
 545 550 555 560
 His Arg Ile Leu Gly Val Ile Tyr Ala Lys Gly Trp Thr Ile Thr Ala
 565 570 575
 Ala Arg Met Leu Ala Asn Gly Gln Trp Ser Ala Glu Phe Asp Val Arg
 580 585 590
 Ala Asn Gly Pro Gln Asp Phe Asp Pro Gln His Phe Leu Gln Ala Tyr

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Gln	Ser	Gly	val	Phe	Ser	Glu	Val	Pro	Ile	Pro	Ala	Pro	Gly	Ile	Thr
595						600						605			
610						615						620			
Ala	Thr	Phe	Trp	His	Gly	Asn	Thr	Leu	Glu	Val	Arg	Thr	Glu	Leu	Arg
625						630					635			640	
Thr	Gly	Ala	Ile	Phe	Ala	Leu	Leu	Arg	Thr	Leu	Pro	Asp	Ala	Leu	Trp
									645	650			655		
Ile	Asn	Ala	Val	Thr	Arg	Gly	Ala	Thr	Leu	Ile	Ile	Gln	Ala	Ala	Leu
									660	665			670		
Lys	Pro	Gly	Phe	Asp	Arg	Ala	Thr	Val	Glu	Arg	Ser	Val	Val	Arg	Ser
								675	680			685			
Leu	Ala	Gly	Ser												
															690